

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

10/525,456

Source:

IPW/16

Date Processed by STIC:

5/5-06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 05/15/2006

PATENT APPLICATION: US/10/525,456

TIME: 15:38:01

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\05152006\J525456.raw

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4 <110> APPLICANT: DIXON, Katharine H
5     LIAU, Gene
6     SERDIKOFF, Cynthia
8 <120> TITLE OF INVENTION: HB-954 AS A TARGET FOR MODULATING
9     ANGIOGENESIS
11 <130> FILE REFERENCE: 4-32303A/USN/GTI
13 <140> CURRENT APPLICATION NUMBER: 10/525,456
14 <141> CURRENT FILING DATE: 2005-05-10
16 <150> PRIOR APPLICATION NUMBER: 60/407,063
17 <151> PRIOR FILING DATE: 2002-08-30
19 <150> PRIOR APPLICATION NUMBER: PCT/EP03/009619
20 <151> PRIOR FILING DATE: 2003-08-29
22 <160> NUMBER OF SEQ ID NOS: 2
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 510
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: PEPTIDE
33 <222> LOCATION: (1)...(510)
34 <223> OTHER INFORMATION: Amino acid sequence of HB-954
36 <400> SEQUENCE: 1
37 Met Gly His Asn Gly Ser Trp Ile Ser Pro Asn Ala Ser Glu Pro His
38 1           5           10           15
39 Asn Ala Ser Gly Ala Glu Ala Ala Gly Val Asn Arg Ser Ala Leu Gly
40           20           25           30
41 Glu Phe Gly Glu Ala Gln Leu Tyr Arg Gln Phe Thr Thr Thr Val Gln
42           35           40           45
43 Trp Ile Phe Ile Gly Ser Leu Leu Gly Asn Phe Met Val Leu Trp Ser
44           50           55           60
45 Thr Cys Arg Thr Thr Val Phe Lys Ser Val Thr Asn Arg Phe Ile Lys
46 65           70           75           80
47 Asn Leu Ala Cys Ser Gly Ile Cys Ala Ser Leu Val Cys Val Pro Phe
48           85           90           95
49 Asp Ile Ile Leu Ser Thr Ser Pro His Cys Cys Trp Trp Ile Tyr Thr
50           100          105          110
51 Met Leu Phe Cys Lys Trp Lys Phe Leu His Lys Val Phe Cys Ser Val
52           115          120          125
53 Thr Ile Leu Ser Phe Pro Ala Ile Ala Leu Asp Arg Tyr Tyr Ser Val
54           130          135          140
55 Leu Tyr Pro Leu Glu Arg Lys Ile Ser Asp Ala Lys Ser Arg Glu Leu
56 145          150          155          160

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57 Val Met Tyr Ile Trp Ala His Ala Trp Ala Ser Val Pro Val Phe Ala
58                      165                      170                      175
59 Val Thr Asn Val Ala Asp Ile Tyr Ala Thr Ser Thr Cys Thr Glu Val
60                      180                      185                      190
61 Trp Ser Asn Ser Leu Gly His Leu Val Tyr Val Leu Val Tyr Asn Ile
62                      195                      200                      205
63 Thr Thr Val Ile Val Pro Val Trp Val Phe Leu Phe Leu Ile Leu Ile
64                      210                      215                      220
65 Arg Arg Ala Leu Ser Ala Ser Gln Lys Lys Lys Val Ile Ile Ala Ala
66 225                      230                      235                      240
67 Leu Arg Thr Pro Gln Asn Thr Ile Ser Ile Pro Tyr Ala Ser Gln Arg
68                      245                      250                      255
69 Glu Ala Glu Leu His Ala Thr Leu Leu Ser Met Val Met Val Phe Ile
70                      260                      265                      270
71 Leu Cys Ser Val Pro Tyr Ala Thr Leu Trp Tyr Gln Thr Val Leu Asn
72                      275                      280                      285
73 Val Pro Asp Thr Ser Val Phe Leu Leu Leu Thr Ala Val Trp Leu Pro
74                      290                      295                      300
75 Lys Val Ser Leu Leu Ala Asn Pro Val Leu Phe Leu Thr Val Asn Lys
76 305                      310                      315                      320
77 Ser Val Arg Lys Cys Leu Ile Gly Thr Leu Val Gln Leu His His Arg
78                      325                      330                      335
79 Tyr Ser Arg Arg Asn Val Val Ser Thr Gly Ser Gly Met Ala Glu Ala
80                      340                      345                      350
81 Ser Leu Glu Pro Ser Ile Arg Ser Gly Ser Gln Leu Leu Glu Met Phe
82                      355                      360                      365
83 His Ile Gly Gln Gln Gln Ile Phe Lys Pro Thr Glu Asp Glu Glu Glu
84                      370                      375                      380
85 Ser Glu Ala Lys Tyr Ile Gly Ser Ala Asp Phe Gln Ala Lys Glu Ile
86 385                      390                      395                      400
87 Phe Ser Thr Cys Leu Glu Gly Glu Gln Gly Pro Gln Phe Ala Pro Ser
88                      405                      410                      415
89 Ala Pro Pro Leu Ser Thr Val Asp Ser Val Ser Gln Val Ala Pro Ala
90                      420                      425                      430
91 Ala Pro Val Glu Pro Glu Thr Phe Pro Asp Lys Tyr Ser Leu Gln Phe
92                      435                      440                      445
93 Gly Phe Gly Pro Phe Glu Leu Pro Pro Gln Trp Leu Ser Glu Thr Arg
94                      450                      455                      460
95 Asn Ser Lys Lys Arg Leu Leu Pro Pro Leu Gly Asn Thr Pro Glu Glu
96 465                      470                      475                      480
97 Leu Ile Gln Thr Lys Val Pro Lys Val Gly Arg Val Glu Arg Lys Met
98                      485                      490                      495
99 Ser Arg Asn Asn Lys Val Ser Ile Phe Pro Lys Val Asp Ser
100                      500                      505                      510
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 2816
105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
108 <220> FEATURE:

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113 <221> NAME/KEY: CDS
114 <222> LOCATION: (867)...(2414)
115 <223> OTHER INFORMATION: Coding sequence
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120 ggggtcccgct gcgcagtgct gaggcaggag gtcggagcca caagtgagg gctgggaagc 180
121 aggaccagc acgggcgtct tggcaggcgg ccggggcgag ggccaggctg ctggggacgc 240
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123 cgccactcg gcgtgggcat tacgttggct tcacatcgcc atccagctc gaagccaaca 360
124 ggactgaaaa atagcttcgg ccaaagctt cctcccgt aaggagagg gtcgagtgcg 420
125 tcagcccgag gggactggag agggatgccc tagccctga gggcgagg acccgcggtt 480
126 gaaggaggca gcgggagcgg agagcgccct ccttgacct cgaatgcctc cttctgtgtt 540
127 tccattctcg tcgagtgggc tgggccacgc tgaccacct ggaggaggga cggacgacgc 600
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149 tagggaccct ggtgcaacta caccaccgg acagtcgccc taatgtggtc agtacaggga 1920
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159 accagagtgt gggaatgctg tggccatgtg attgtatgat ctcttgcaa ctcagtgtga 2520

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163 taccocatgt gcactttctg aggatgcctc acttccctgg gctctgcaga gaacacacag 2760
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/525,456

DATE: 05/15/2006

TIME: 15:38:02

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